



0500/02

# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/038,717  
Source: 01PE  
Date Processed by STIC: 1/28/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

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Please consider using alternative methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002



OIPE

## RAW SEQUENCE LISTING

DATE: 01/28/2002

PATENT APPLICATION: US/10/038,717

TIME: 18:08:34

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01282002\J038717.raw

Does Not Comply  
Corrected Diskette Needed

29 <110> APPLICANT: HITACHI, LTD.  
 W--> 30 <120> TITLE OF INVENTION: Method of DNA Sequencing, Reagent Kit for DNA  
 W--> 31 Sequencing and Apparatus for DNA Sequencing  
 W--> 32 <130> FILE REFERENCE: NT01P0333  
 W--> 33 <140> CURRENT APPLICATION NUMBER: US/10/038,717  
 W--> 33 <141> CURRENT FILING DATE: 2002-01-08  
 W--> 33 <160> NUMBER OF SEQ ID: 12

## ERRORED SEQUENCES

158 <210> SEQ ID NO: 12  
 159 <211> LENGTH: 20  
 160 <212> TYPE: DNA  
 161 <213> ORGANISM: Artificial Sequence  
 W--> 162 <220> FEATURE:  
 W--> 162 <223> OTHER INFORMATION: DNA primer complementary with base sequence  
 W--> 165 <400> SEQUENCE: 12  
 166 ggtctctctccc aggacaggca  
 W--> 170 SEQUENCE LISTING FREE TEXT  
 W--> 171 (1) Description on another data concerning the sequence  
 E--> 172 of sEQ Id nO: 1  
 E--> 173 template dna originating from ml3mp18.  
 W--> 174 (2) Another data concerning the sequence of SEQ ID NO:  
 W--> 175 2  
 E--> 176 dna primer complementary with base sequence between 88  
 E--> 177 and 105 from the 5' terminus of sEQ Id nO: 1, having 17  
 W--> 178 bases, having the 15-th base C from the 5' terminus of  
 W--> 179 this DNA primer replaced by G for introducing a  
 W--> 180 mismatch between DNA primer and template DNA, and being  
 W--> 181 able to be extended.  
 W--> 182 (3) Another data concerning the sequence of SEQ ID NO:  
 W--> 183 3  
 E--> 184 dna primer complementary with base sequence between 88  
 E--> 185 and 105 from the 5' terminus of sEQ Id nO: 1, having 17  
 W--> 186 bases, having the 15-th base C from the 5' terminus of  
 W--> 187 this DNA primer replaced by G for introducing a  
 W--> 188 mismatch between DNA primer and template DNA, and being  
 W--> 189 not able to be extended.  
 W--> 190 (4) Another data concerning the sequence of SEQ ID NO:  
 W--> 191 4  
 E--> 192 dna primer complementary with base sequence between 88  
 E--> 193 and 105 from the 5' terminus of sEQ Id nO: 1, having 17

20

(see next page)  
 This section is invalid.  
 DO NOT add any text after the last sequence. Please incorporate this information into the relevant sequences in the <2207-2237> section.  
 <2237> response has a MAXIMUM of 4 lines

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W--> 194 bases, and being able to be extended.  
W--> 195 (5) Another data concerning the sequence of SEQ ID NO:  
W--> 196 5  
W--> 197 Template DNA originating from p53 and including base  
E--> 198 sequence of exon 8.  
W--> 199 (6) Another data concerning the sequence of SEQ ID NO:  
W--> 200 6  
E--> 201 dna primer complementary with base sequence between 55  
E--> 202 and 76 from the 5' terminus of sEQ Id nO: 5, having 22  
W--> 203 bases, having the 19-th base T from the 5' terminus of  
W--> 204 this DNA primer replaced by A for introducing a  
W--> 205 mismatch between DNA primer and template DNA, and being  
W--> 206 able to be extended.  
W--> 207 (7) Another data concerning the sequence of SEQ ID NO:  
W--> 208 7  
W--> 209 Template DNA originating from p53 and having the 55-th  
W--> 210 base A from the 5' terminus of this DNA primer replaced  
W--> 211 by A.  
W--> 212 (8) Another data concerning the sequence of SEQ ID NO:  
W--> 213 8  
E--> 214 dna primer complementary with base sequence between 55  
E--> 215 and 76 from the 5' terminus of sEQ Id nO: 7, having 22  
W--> 216 bases, having the 19-th base T from the 5' terminus of  
W--> 217 this DNA primer replaced by A for introducing a  
W--> 218 mismatch between DNA primer and template DNA, and being  
W--> 219 able to be extended.  
W--> 220 (9) Another data concerning the sequence of SEQ ID NO:  
W--> 221 9  
E--> 222 dna primer complementary with base sequence between 55  
E--> 223 and 76 from the 5' terminus of sEQ Id nO: 5 and 7,  
E--> 224 having 22 bases, having the 19-th base t from the 5'  
W--> 225 terminus of this DNA primer replaced by A for  
W--> 226 introducing a mismatch between DNA primer and template  
W--> 227 DNA, and being not able to be extended.  
W--> 228 (10) Another data concerning the sequence of SEQ ID NO:  
W--> 229 10  
E--> 230 dna primer complementary with base sequence between 55  
E--> 231 and 76 from the 5' terminus of sEQ Id nO: 5 and 7,  
E--> 232 having 22 bases, having the 19-th base t from the 5'  
W--> 233 terminus of this DNA primer replaced by A for  
W--> 234 introducing a mismatch between DNA primer and template  
W--> 235 DNA, and being not able to be extended.  
W--> 236 (11) Another data concerning the sequence of SEQ ID NO:  
W--> 237 11  
W--> 238 Template DNA originating from p53 and including base  
E--> 239 sequence of exon 8.  
W--> 240 (12) Another data concerning the sequence of SEQ ID NO:  
W--> 241 12  
E--> 242 dna primer complementary with base sequence between 44

*same  
end*

*see  
p. 3*

## RAW SEQUENCE LISTING

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E--> 243 and 63 from the 5' terminus of SEQ Id n0: 11, having 20  
W--> 244 bases, and DNA primer being able to be extended.

E--> 245 Page 1

E--> 249 14

E--> 251 1

*delete**same*

*see following pages for more error*

<210> 2  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence  
 <220>

<223> DNA primer complementary with base sequence  
 between 88 and 105 of SEQ ID NO:1, but the base  
 replaced C at 15 of this DNA primer by G for  
 introducing a mismatch between DNA primer and template  
 DNA, and DNA primer being able to be extended  
 <400> 2

Per Sequence Rules,

<2237 response has a  
maximum of 4 lines

add

↓

<2237

→ <2207

insert  
 a <2207 after  
4th line,  
 and add <2237  
 at beginning  
 of 5<sup>th</sup> line

10/038,717 5

<210> 3

<211> 17

<212> DNA

<213> Artificial Sequence

<223> DNA primer complementary with base sequence

> C2207 add this

mandatory.

rename identifier

whenever C2217, C2227,

or C2237 is shown

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Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01282002\J038717.raw

L:30 M:283 W: Missing Blank Line separator, <120> field identifier  
L:32 M:283 W: Missing Blank Line separator, <130> field identifier  
L:33 M:270 C: Current Application Number differs, Replaced Current Application No  
L:33 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:33 M:283 W: Missing Blank Line separator, <160> field identifier  
L:34 M:283 W: Missing Blank Line separator, <210> field identifier  
L:38 M:283 W: Missing Blank Line separator, <220> field identifier  
L:40 M:283 W: Missing Blank Line separator, <400> field identifier  
L:48 M:283 W: Missing Blank Line separator, <220> field identifier  
L:53 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:54 M:283 W: Missing Blank Line separator, <400> field identifier  
L:60 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:64 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:65 M:283 W: Missing Blank Line separator, <400> field identifier  
L:71 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:74 M:283 W: Missing Blank Line separator, <400> field identifier  
L:80 M:283 W: Missing Blank Line separator, <220> field identifier  
L:83 M:283 W: Missing Blank Line separator, <400> field identifier  
L:91 M:283 W: Missing Blank Line separator, <220> field identifier  
L:96 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:97 M:283 W: Missing Blank Line separator, <400> field identifier  
L:103 M:283 W: Missing Blank Line separator, <220> field identifier  
L:107 M:283 W: Missing Blank Line separator, <400> field identifier  
L:115 M:283 W: Missing Blank Line separator, <220> field identifier  
L:120 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:121 M:283 W: Missing Blank Line separator, <400> field identifier  
L:127 M:283 W: Missing Blank Line separator, <220> field identifier  
L:132 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:133 M:283 W: Missing Blank Line separator, <400> field identifier  
L:139 M:283 W: Missing Blank Line separator, <220> field identifier  
L:144 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:145 M:283 W: Missing Blank Line separator, <400> field identifier  
L:151 M:283 W: Missing Blank Line separator, <220> field identifier  
L:154 M:283 W: Missing Blank Line separator, <400> field identifier  
L:162 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:165 M:283 W: Missing Blank Line separator, <400> field identifier  
L:170 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:171 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
L:172 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:172 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:172 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:30 SEQ:12  
L:172 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7  
L:172 M:112 C: (48) String data converted to lower case,  
L:173 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:173 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12

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Input Set : A:\PTO.VSK.txt

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L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
M:254 Repeated in SeqNo=12  
L:173 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16  
M:112 Repeated in SeqNo=12  
L:174 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:176 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:176 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:176 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
L:177 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:177 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:177 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20  
L:178 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
L:178 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:179 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
L:179 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:180 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
L:180 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:181 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
L:181 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:182 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
L:182 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:184 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:184 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:184 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
L:185 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:185 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:185 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20  
L:186 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
L:186 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:187 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
L:187 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:188 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
L:188 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:189 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:189 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5  
L:189 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12



VERIFICATION SUMMARY

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L:190 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
 L:190 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
 L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
 L:192 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
 L:192 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
 L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
 L:192 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
 L:193 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
 L:193 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
 L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
 L:193 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20  
 L:194 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
 L:194 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
 L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
 L:195 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
 L:195 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
 L:196 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
 L:197 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
 L:197 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
 L:198 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
 L:198 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
 L:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
 L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
 L:198 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:199 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
 L:199 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
 L:200 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
 L:201 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
 L:201 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
 L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
 L:201 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
 L:202 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
 L:202 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
 L:202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
 L:202 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:19  
 L:203 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
 L:203 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
 L:204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
 L:204 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
 L:204 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
 L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
 L:205 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
 L:205 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
 L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
 L:206 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
 L:206 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
 L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
 L:207 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
 L:207 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12

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L:208 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:209 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
L:209 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:210 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
L:210 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:211 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
L:211 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:212 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:212 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
L:212 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:214 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:214 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:214 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
L:215 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:215 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:215 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:19  
L:216 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
L:216 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:217 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
L:217 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:218 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
L:218 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:219 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
L:219 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:220 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
L:220 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:222 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:222 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:222 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
L:223 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:223 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:223 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:223 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:19  
L:224 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:224 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:224 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/038,717

DATE: 01/28/2002

TIME: 18:08:35

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01282002\J038717.raw

L:225 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
L:225 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:226 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
L:226 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:227 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
L:227 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:228 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
L:228 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:230 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:230 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:230 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
L:231 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:231 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:231 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:231 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:19  
L:232 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:232 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:232 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16  
L:233 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
L:233 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:234 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
L:234 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:235 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
L:235 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:236 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:236 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
L:236 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:238 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
L:238 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:239 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:239 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:239 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
L:240 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
L:240 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:242 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:242 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/038,717

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Input Set : A:\PTO.VSK.txt

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L:242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:242 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
L:243 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:243 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:243 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20  
L:244 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
L:244 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 12  
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:245 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:251 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:810 SEQ:12